

								37 m	38 m	40 m	45 m	60 m	60 m	65 m	65 m	65 m	70 m	75 m	80 m
#OTU ID	Kingdom	Phylum	Class	Order	Family	genus	species	SAI261	SAI265	SAI178	SAI134	SAI237	SAI239	SAI244	SAI251	SAI229	SAI101	SAI211	SAI116
OTU_83	k__Archaea	p__Crenarchaeota	c__Thaumarchaeota	o__Cenarchaeales	f__Cenarchaeaceae	g__Nitrosopumilus	s__	11	0	4	17	26	1	51	47	1	19	33	8
OTU_5	k__Archaea	p__Crenarchaeota	c__Thaumarchaeota	o__Cenarchaeales	f__Cenarchaeaceae	g__Cenarchaeum	s__symbiosum	10	1	40	1160	0	0	285	0	7	0	0	12
OTU_2	k__Archaea	p__Crenarchaeota	c__Thaumarchaeota	o__Cenarchaeales	f__Cenarchaeaceae	g__Cenarchaeum	s__symbiosum	0	0	8	5	0	0	44	72	0	3458	0	3
OTU_202	k__Archaea	p__Crenarchaeota	c__Thaumarchaeota	o__Cenarchaeales	f__Cenarchaeaceae	g__	s__	0	0	0	2	0	0	1	0	1	7	0	0
OTU_73	k__Archaea	p__Crenarchaeota	c__Thaumarchaeota	o__Cenarchaeales	f__Cenarchaeaceae	g__	s__	0	0	0	0	0	0	41	14	0	0	0	3
OTU_365	k__Bacteria	p__Acidobacteria	c__Acidobacteria-6	o__BPC015	f__	g__	s__	0	2	0	1	15	0	3	0	0	2	4	0
OTU_107	k__Bacteria	p__Acidobacteria	c__Acidobacteria-6	o__BPC015	f__	g__	s__	5	0	1	0	0	0	5	19	0	0	0	2
OTU_1853	k__Bacteria	p__Acidobacteria	c__Acidobacteria-6	o__BPC015	f__	g__	s__	0	0	0	0	1	0	2	0	0	1	0	2
OTU_182	k__Bacteria	p__Acidobacteria	c__Acidobacteria-6	o__iii1-15	f__	g__	s__	0	0	1	0	0	0	10	12	0	1	0	3
OTU_186	k__Bacteria	p__Acidobacteria	c__Acidobacteria-6	o__iii1-15	f__	g__	s__	0	0	0	0	0	0	4	2	0	0	0	12
OTU_160	k__Bacteria	p__Acidobacteria	c__PAUC37f	o__	f__	g__	s__	0	0	0	0	0	0	9	24	0	0	0	1
OTU_385	k__Bacteria	p__Acidobacteria	c__Sva0725	o__Sva0725	f__	g__	s__	0	5	0	6	8	0	11	0	0	1	7	3
OTU_136	k__Bacteria	p__Acidobacteria	c__Sva0725	o__Sva0725	f__	g__	s__	0	0	0	0	0	0	9	44	0	2	0	0
OTU_509	k__Bacteria	p__Acidobacteria	c__Sva0725	o__Sva0725	f__	g__	s__	0	3	0	1	0	0	4	0	0	0	0	0
OTU_929	k__Bacteria	p__Acidobacteria	c__Sva0725	o__Sva0725	f__	g__	s__	0	1	0	2	0	0	1	0	0	0	0	0
OTU_132	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__	5	0	0	45	0	0	17	0	0	0	0	0
OTU_77	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__	17	0	0	0	1	0	0	0	0	2	0	0
OTU_460	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__JdFBGBact	g__	s__	2	5	0	0	6	0	3	2	0	0	1	0
OTU_605	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__JdFBGBact	g__	s__	0	14	0	0	1	0	0	0	0	0	3	0
OTU_342	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__ntu14	g__	s__	1	4	0	0	0	0	4	0	0	0	2	1
OTU_1120	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__SC3-41	g__	s__	0	4	0	0	0	0	1	0	0	0	1	0
OTU_225	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__wb1_P06	g__	s__	4	0	3	0	0	0	2	7	0	0	0	1
OTU_421	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__wb1_P06	g__	s__	0	11	0	0	0	0	2	10	0	0	0	0
OTU_192	k__Bacteria	p__AncK6	c__	o__	f__	g__	s__	7	0	0	0	0	0	14	16	0	0	0	0
OTU_287	k__Bacteria	p__Bacteroidetes	c__[Rhodothermi]	o__[Rhodothermales]	f__[Balneolaceae]	g__Balneola	s__	0	11	0	1	0	0	12	0	0	0	0	0
OTU_917	k__Bacteria	p__Bacteroidetes	c__[Rhodothermi]	o__[Rhodothermales]	f__[Balneolaceae]	g__Balneola	s__	0	4	0	2	0	0	0	0	0	0	1	0
OTU_686	k__Bacteria	p__Bacteroidetes	c__[Rhodothermi]	o__[Rhodothermales]	f__Rhodothermaceae	g__	s__	1	0	0	0	2	0	1	5	0	1	0	0
OTU_1497	k__Bacteria	p__Bacteroidetes	c__[Rhodothermi]	o__[Rhodothermales]	f__Rhodothermaceae	g__	s__	0	1	0	1	2	0	5	0	0	0	0	0
OTU_339	k__Bacteria	p__Bacteroidetes	c__[Rhodothermi]	o__[Rhodothermales]	f__Rhodothermaceae	g__	s__	0	6	0	2	0	0	1	0	0	0	7	0
OTU_441	k__Bacteria	p__Bacteroidetes	c__[Saprospirae]	o__[Saprospirales]	f__Saprospiraceae	g__	s__	0	1	2	0	0	0	0	0	0	0	9	0
OTU_455	k__Bacteria	p__Bacteroidetes	c__[Saprospirae]	o__[Saprospirales]	f__Saprospiraceae	g__	s__	11	8	0	0	0	0	0	0	0	0	1	0
OTU_352	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__[Amoebophilaceae]	g__	s__	2	1	0	0	9	1	7	0	0	0	0	0
OTU_187	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__[Amoebophilaceae]	g__	s__	3	0	0	0	25	0	1	0	0	0	19	0
OTU_126	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__[Amoebophilaceae]	g__SGUS912	s__	0	177	1	0	0	8	0	0	0	0	0	0
OTU_471	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__[Amoebophilaceae]	g__Ucs1325	s__	0	14	0	2	0	0	0	0	0	0	5	0
OTU_296	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	1	4	0	3	2	0	7	16	0	0	2	0
OTU_109	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	1	10	0	6	1	0	0	0	0	0	0	0
OTU_135	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__Roseivirga	s__	0	5	0	0	0	0	2	98	0	0	2	0
OTU_154	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	2	0	1	0	0	3	0	0	0	61	0
OTU_3112	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	6	1	0	0	0	4	0	0	1	0	0
OTU_831	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__Roseivirga	s__	0	3	0	1	1	2	0	0	0	0	0	0
OTU_2940	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	2	0	2	0	0	0	0	0	0	1	0
OTU_417	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	3	0	3	0	0	2	0	0	0	0	0
OTU_535	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	4	0	3	0	0	1	0	0	0	0	0
OTU_616	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	7	1	0	0	0	2	0	0	0	0	0
OTU_975	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__	0	0	0	1	2	0	3	0	0	0	0	0
OTU_734	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__	g__	s__	0	7	0	0	1	0	1	0	0	0	0	0
OTU_748	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__[Weeksellaceae]	g__Elizabethkingia	s__meningoseptica	9	0	0	0	1	0	0	2	0	0	0	0
OTU_256	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__	s__	19	0	1	0	3	0	0	9	2	0	0	9
OTU_274	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__	s__	0	2	0	1	0	0	2	0	0	0	9	0
OTU_190	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__	s__	0	0	0	2	0	0	4	0	0	0	26	0
OTU_357	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__	s__	0	13	0	1	0	0	0	0	0	0	15	0
OTU_514	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__	s__	0	1	0	0	0	0	0	0	6	0	3	0

OTU_697	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__Muricauda	s__	0	0	0	0	1	0	2	2	0	0	0	0
OTU_762	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__Muricola	s__jejuensis	0	2	0	1	6	0	0	0	0	0	0	0
OTU_222	k__Bacteria	p__Bacteroidetes						34	1	1	0	4	0	2	0	18	0	0	23
OTU_465	k__Bacteria	p__Caldithrix	c__Caldithrixae	o__Caldithrixales				0	0	0	0	2	0	2	0	0	0	1	0
OTU_838	k__Bacteria	p__Chlorobi						2	0	0	1	0	0	0	0	0	0	0	1
OTU_1722	k__Bacteria	p__Chloroflexi	c__Anaerolineae	o__Caldilineales	f__Caldilineaceae	g__	s__	0	1	0	0	0	0	1	0	0	0	2	0
OTU_101	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	0	0	0	0	0	0	37	13	0	1	0	3
OTU_84	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	0	0	1	0	0	0	38	42	0	0	0	2
OTU_180	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	0	0	0	0	0	0	8	2	0	4	0	0
OTU_392	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	0	0	0	0	0	0	4	6	3	0	0	0
OTU_474	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	1	0	0	0	0	0	7	5	0	0	0	0
OTU_834	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	4	0	0	1	0	0	0	3	0	0	0	0
OTU_99	k__Bacteria	p__Chloroflexi	c__SAR202	o__	f__	g__	s__	0	0	1	0	0	0	5	10	0	0	0	0
OTU_52	k__Bacteria	p__Cyanobacteria	c__Synechococcophycideae	o__Pseudanabaenales	f__Pseudanabaenaceae	g__	s__	17	88	0	5	0	0	0	0	0	0	0	3
OTU_253	k__Bacteria	p__Cyanobacteria	c__Synechococcophycideae	o__Synechococcales	f__Acaryochloridaceae	g__Acaryochloris	s__	0	1	0	1	3	0	1	0	0	0	0	0
OTU_241	k__Bacteria	p__Cyanobacteria	c__Synechococcophycideae	o__Synechococcales	f__Synechococcaceae	g__Synechococcus	s__	0	0	0	5	2	0	2	0	0	1	0	4
OTU_289	k__Bacteria	p__Cyanobacteria	c__Synechococcophycideae	o__Synechococcales	f__Synechococcaceae	g__Prochlorococcus	s__	1	2	0	16	1	0	2	0	0	0	0	0
OTU_1617	k__Bacteria	p__Firmicutes	c__Bacilli	o__Lactobacillales	f__Enterococcaceae	g__Enterococcus	s__	0	0	1	0	0	0	0	0	3	0	0	2
OTU_426	k__Bacteria	p__Firmicutes	c__Bacilli	o__Lactobacillales	f__Streptococcaceae	g__Streptococcus	s__	2	0	1	1	0	0	0	0	0	0	0	15
OTU_223	k__Bacteria	p__Gemmatimonadetes	c__Gemm-2	o__	f__	g__	s__	0	0	0	0	2	0	5	0	0	0	3	0
OTU_201	k__Bacteria	p__Gemmatimonadetes	c__Gemm-4	o__	f__	g__	s__	0	0	0	0	0	0	1	110	0	0	1	0
OTU_323	k__Bacteria	p__Lentisphaerae	c__[Lentisphaeria]	o__Lentisphaerales	f__Lentisphaeraceae	g__	s__	0	5	0	2	0	0	0	0	0	0	1	0
OTU_219	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	0	0	0	6	2	0	4	0	0	3	27	0
OTU_40	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	0	1	2	0	0	0	24	53	0	1	0	0
OTU_754	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	0	0	0	5	0	0	1	4	0	0	4	0
OTU_1205	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	0	0	0	1	1	0	0	0	0	0	1	0
OTU_3127	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	0	0	0	1	0	0	0	0	0	1	1	0
OTU_696	k__Bacteria	p__Nitrospirae	c__Nitrospira	o__Nitrospirales	f__Nitrospiraceae	g__	s__	5	0	0	1	0	0	1	0	0	0	0	0
OTU_162	k__Bacteria	p__PAUC34f	c__	o__	f__	g__	s__	0	0	0	0	0	0	13	52	1	0	0	2
OTU_957	k__Bacteria	p__PAUC34f	c__	o__	f__	g__	s__	5	0	0	0	0	0	0	8	0	0	0	4
OTU_384	k__Bacteria	p__Planctomycetes	c__OM190	o__CL500-15	f__	g__	s__	0	3	0	3	0	0	3	0	0	0	1	0
OTU_1126	k__Bacteria	p__Planctomycetes	c__OM190	o__CL500-15	f__	g__	s__	0	3	0	0	0	0	0	0	0	1	1	0
OTU_245	k__Bacteria	p__Planctomycetes	c__Phycisphaerae	o__Phycisphaerales	f__Phycisphaeraceae	g__	s__	6	9	0	2	1	0	8	6	0	0	0	0
OTU_950	k__Bacteria	p__Planctomycetes	c__Phycisphaerae	o__Phycisphaerales	f__Phycisphaeraceae	g__	s__	0	0	0	0	1	0	2	0	0	1	0	0
OTU_1036	k__Bacteria	p__Planctomycetes	c__Pla3	o__	f__	g__	s__	0	0	0	0	1	0	2	8	0	1	0	0
OTU_450	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__Planctomycete	s__LF1	0	8	0	1	4	0	1	26	0	0	4	0
OTU_636	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	1	1	0	2	0	0	1	0	0	0	1	0
OTU_698	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	3	0	2	2	0	2	0	0	0	2	0
OTU_224	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	5	0	0	3	0	1	0	0	0	7	0
OTU_477	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	1	0	1	3	0	3	0	0	0	0	0
OTU_1541	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	2	0	1	0	0	0	0	0	0	1	0
OTU_1657	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	1	0	1	0	0	0	0	0	0	1	0
OTU_578	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	0	0	1	0	0	1	0	0	0	0	3
OTU_607	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	3	0	1	2	0	0	0	0	0	0	0
OTU_684	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	0	0	2	0	0	3	0	0	0	5	0
OTU_767	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	3	0	2	3	0	0	0	0	0	0	0
OTU_827	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	3	0	0	1	0	5	0	0	0	0	0
OTU_952	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__	0	6	0	1	0	0	0	3	0	0	0	0
OTU_85	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__	f__	g__	s__	0	51	1	14	2	0	8	9	0	2	16	0
OTU_337	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__	f__	g__	s__	0	7	0	3	0	0	3	0	0	0	2	0
OTU_1143	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__	f__	g__	s__	0	0	1	0	0	0	1	0	0	0	0	3
OTU_353	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__	f__	g__	s__	2	0	0	1	4	0	0	0	0	0	0	0
OTU_396	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__	f__	g__	s__	2	0	0	0	10	0	1	0	0	0	0	0
OTU_41	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kiloniellales	f__	g__	s__	0	8	0	6	1	0	97	0	0	1	83	1
OTU_215	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kiloniellales	f__	g__	s__	0	2	0	13	2	0	117	0	0	0	1	2

OTU_804	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kiloniellales	f__	g__	s__	0	4	0	1	4	0	5	0	0	0	0	0
OTU_391	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kiloniellales	f__	g__	s__	0	0	0	1	0	0	1	0	0	0	10	0
OTU_115	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kordiimonadales	f__Kordiimonadaceae	g__	s__	0	1	0	7	1	0	19	1	0	0	0	0
OTU_239	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kordiimonadales	f__Kordiimonadaceae	g__	s__	0	3	0	9	0	0	1	0	0	0	0	0
OTU_1026	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Bradyrhizobiaceae	g__Bradyrhizobium	s__	11	0	0	0	1	0	0	5	0	0	0	2
OTU_211	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Cohaesibacteriaceae	g__Cohaesibacter	s__	0	5	0	1	0	0	3	0	0	0	0	0
OTU_141	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	39	3	2	5	0	1	0	0	2	1	0
OTU_412	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	1	18	1	1	0	0	3	0	0	0	3	0
OTU_106	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	8	0	8	15	0	5	0	0	0	3	0
OTU_3678	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	2	0	2	4	0	1	0	0	6	0	0
OTU_318	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	2	0	0	1	0	2	0	0	0	17	0
OTU_114	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	0	0	0	1	0	2	0	3	0	0	0
OTU_247	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Hyphomicrobiaceae	g__	s__	0	0	0	0	0	0	0	0	0	1	1	2
OTU_28	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Phyllobacteriaceae	g__	s__	4	28	1	6	6	0	107	15	0	3	123	2
OTU_634	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Phyllobacteriaceae	g__	s__	0	13	0	1	0	0	2	0	0	0	1	0
OTU_2608	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Phyllobacteriaceae	g__Chelativorans	s__	0	0	0	0	1	0	2	0	0	0	2	0
OTU_429	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__	g__	s__	0	2	0	0	0	0	1	0	0	0	1	0
OTU_249	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Hyphomonadaceae	g__Hyphomonas	s__	0	28	0	2	0	0	1	0	0	0	3	0
OTU_32	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	1	124	3	13	12	1	25	61	0	3	157	32
OTU_12	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	17	3	21	680	0	0	66	0	0	0	0	10
OTU_218	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	30	1	1	1	0	0	18	0	0	5	0
OTU_727	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Loktanella	s__	0	6	0	0	4	0	1	11	0	0	1	8
OTU_267	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	58	1	9	0	0	1	2	0	0	0	0
OTU_867	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Roseovarius	s__	0	0	0	0	1	0	2	1	3	0	0	2
OTU_1300	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	1	0	1	0	0	0	0	0	0	1	1
OTU_1360	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Paracoccus	s__	0	0	0	0	1	0	0	4	1	0	0	1
OTU_439	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	9	0	0	0	0	1	16	0	0	11	0
OTU_614	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	3	0	1	1	0	2	0	0	0	0	0
OTU_830	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__	s__	0	0	0	0	1	0	1	0	3	0	4	0
OTU_110	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__	g__	s__	0	50	1	6	5	0	7	2	0	2	1	0
OTU_234	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__	g__	s__	2	7	0	0	39	1	0	0	0	0	0	6
OTU_242	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__	g__	s__	0	18	0	3	2	0	4	0	0	1	0	0
OTU_10	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Inquilinus	s__	72	4	4	39	91	1	74	85	0	17	8	5
OTU_33	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Rhodovibrio	s__	1	25	2	8	4	0	9	21	0	1	25	0
OTU_16	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Rhodovibrio	s__	7	0	4	12	7	0	8	0	0	12	0	2
OTU_402	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	6	0	5	1	0	19	3	0	1	7	0
OTU_49	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	1	1	1	0	0	2	1	0	0	4	1
OTU_68	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	1	7	0	7	55	0	25	0	0	7	0	4
OTU_81	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Rhodovibrio	s__	10	8	0	29	13	0	32	0	0	7	10	0
OTU_9	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	3	41	6	0	56	23	0	10	0	1
OTU_204	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	1	0	1	1	0	0	13	2	0	5	0
OTU_739	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Inquilinus	s__	0	0	0	1	2	0	6	18	0	15	1	0
OTU_26	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	2	1	0	9	5	0	8	0	0
OTU_61	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	1	0	0	8	0	0	6	1	0	1	0	0
OTU_2482	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Rhodovibrio	s__	0	0	0	0	2	0	4	6	0	0	2	0
OTU_272	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Inquilinus	s__	0	16	0	2	0	0	4	18	0	0	0	0
OTU_2792	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Inquilinus	s__	0	0	3	3	1	0	0	0	0	0	5	0
OTU_1216	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	1	0	2	0	0	0	0	0	1	0	0
OTU_1225	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	0	2	1	2	0	0	0	0	0
OTU_199	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Inquilinus	s__	0	0	0	1	0	0	1	9	0	0	0	0
OTU_214	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	1	3	0	1	0	0	0	0	0
OTU_2160	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__Rhodovibrio	s__	0	0	0	3	3	0	0	0	0	1	0	0
OTU_231	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	1	0	1	0	0	3	0	0	0	0	0
OTU_254	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	1	0	0	0	0	1	0	0	0	1	0
OTU_277	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	0	0	0	5	0	0	6	0	5

OTU_340	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	1	0	0	1	0	0	1	0	0
OTU_347	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	0	1	0	2	0	0	0	1	0
OTU_946	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	3	0	0	1	2	0	0	0	0	0	0	0
OTU_98	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Rhodospirillaceae	g__	s__	0	0	0	1	0	0	12	25	0	0	0	0
OTU_512	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Erythrobacteraceae	g__Erythrobacter	s__	0	1	0	0	0	0	0	2	0	0	0	5
OTU_389	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Sphingomonadaceae	g__Sphingomonas	s__	8	1	5	0	0	0	0	0	0	0	0	12
OTU_121	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	2	9	0	5	0	0	0	2	0
OTU_146	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	2	0	2	0	1	0	0	0	1	0
OTU_170	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	1	2	0	2	0	0	1	0	0
OTU_327	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	26	1	0	0	0	2	0	0	0	2	0
OTU_64	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	1	0	0	1	0	0	4	0	3
OTU_1111	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	0	0	0	2	0	0	0	2	1
OTU_1423	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					2	0	0	1	8	0	0	0	0	0	0	0
OTU_1850	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	1	0	0	0	0	0	1	3	0
OTU_677	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	3	0	0	1	0	0	0	5	0
OTU_744	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria					0	0	0	1	0	0	1	0	0	0	1	0
OTU_3	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Burkholderiaceae	g__Burkholderia	s__	184	0	0	0	26	4335	0	0	0	0	0	0
OTU_22	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Oxalobacteraceae	g__Ralstonia	s__	4	0	190	5	2	0	4	250	256	0	21	802
OTU_4	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__EC94	f__	g__	s__	2631	225	773	0	111	48	16	2	1952	0	86	1414
OTU_82	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__[Entotheonellales]	f__[Entotheonellaceae]	g__	s__	4	1	1	0	0	0	40	15	0	2	0	0
OTU_375	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__[Entotheonellales]	f__[Entotheonellaceae]	g__Candidatus Entotheonella	s__	0	0	0	1	1	0	0	0	0	2	1	0
OTU_1355	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__[Entotheonellales]	f__[Entotheonellaceae]	g__Candidatus Entotheonella	s__	0	1	0	0	2	0	0	0	0	0	1	0
OTU_790	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__[Entotheonellales]	f__[Entotheonellaceae]	g__Candidatus Entotheonella	s__	0	6	0	1	2	0	0	0	0	0	0	0
OTU_949	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__[Entotheonellales]	f__[Entotheonellaceae]	g__Candidatus Entotheonella	s__	0	1	1	0	6	0	0	0	0	0	0	0
OTU_23	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Desulfovibrionales				8	0	13	375	0	0	0	0	0	0	0	5
OTU_155	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Myxococcales	f__	g__	s__	1	0	0	3	38	0	15	0	0	4	0	0
OTU_589	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Myxococcales	f__	g__	s__	0	1	0	0	1	0	0	0	0	1	3	0
OTU_1499	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Myxococcales	f__	g__	s__	0	0	0	0	1	0	2	1	0	0	0	0
OTU_1793	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Myxococcales	f__Nannocystaceae	g__Plesiocystis	s__	1	0	0	1	0	0	1	0	0	0	0	0
OTU_97	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__	g__	s__	0	3	0	1	2	0	1	5	0	0	1	0
OTU_485	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__	g__	s__	0	1	0	2	1	0	1	0	0	1	0	0
OTU_282	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__	g__	s__	0	6	0	3	24	0	2	0	0	0	0	0
OTU_718	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__	g__	s__	0	3	0	1	0	0	1	0	0	0	0	0
OTU_144	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__JTB38	g__	s__	0	1	0	3	1	0	27	0	1	1	2	0
OTU_683	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__JTB38	g__	s__	0	1	0	0	3	1	0	0	0	0	0	0
OTU_711	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__JTB38	g__	s__	0	6	0	3	0	0	1	0	0	0	0	0
OTU_1146	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__MND4	g__	s__	0	0	0	1	0	0	0	0	0	1	1	2
OTU_1335	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__MND4	g__	s__	0	2	0	0	0	0	2	0	0	0	1	0
OTU_868	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__NB1-j	f__NB1-i	g__	s__	0	1	0	1	0	0	1	0	0	0	0	0
OTU_157	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Sva0853	f__	g__	s__	107	3	1	0	2	3	1	0	17	0	3	0
OTU_51	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Syntrophobacterales	f__Syntrophobacteraceae	g__	s__	0	0	0	0	2	0	40	10	0	2	0	2
OTU_768	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Syntrophobacterales	f__Syntrophobacteraceae	g__	s__	0	0	0	1	0	0	1	0	0	0	1	0
OTU_845	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Syntrophobacterales	f__Syntrophobacteraceae	g__	s__	0	0	0	0	3	0	1	0	0	1	0	0
OTU_159	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__	f__	g__	s__	0	31	0	3	6	0	18	4	0	1	12	1
OTU_34	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Alteromonas	s__	7	141	16	2	15	12	3	174	63	0	0	14
OTU_169	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Glaciecola	s__	0	20	0	2	3	0	18	24	0	1	6	1
OTU_185	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__nsmpVI18	s__	0	4	0	3	0	0	1	4	0	0	6	0
OTU_95	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__BD2-13	s__	4	0	0	1	49	0	2	13	0	0	0	0
OTU_150	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae			0	0	0	1	0	0	2	1	0	0	10	0
OTU_594	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Spongiibacter	s__	0	0	1	1	1	0	0	8	0	0	0	0
OTU_206	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Candidatus Endobugula	s__	0	2	0	17	0	0	0	0	4	0	0	0
OTU_374	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Marinobacter	s__hydrocarbonoclasticus	0	11	0	0	0	0	1	4	0	0	0	0
OTU_80	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__	s__	0	0	0	0	4	0	4	0	0	0	5	0
OTU_900	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__	s__	0	26	0	2	0	0	0	5	0	0	0	0
OTU_104	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	21	7	1	4	2	0	1	43	4	3	0	0

OTU_124	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	27	16	1	1	0	0	1	8	0	5	0	6
OTU_53	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	112	75	0	9	0	0	0	15	0	2	75	0
OTU_153	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	5	0	1	1	0	0	0	0	0	0	2	1
OTU_2658	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	1	0	0	0	0	0	0	8	0	1	0	0
OTU_271	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Colwelliaceae	g__Thalassomonas	s__	0	1	0	0	0	0	1	3	0	0	0	0
OTU_333	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__HTCC2188	g__HTCC	s__	0	0	0	2	2	0	2	2	0	1	0	0
OTU_366	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__HTCC2188	g__HTCC	s__	0	13	0	2	1	0	3	0	0	0	0	0
OTU_511	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Idiomarinaceae	g__Idiomarina	s__	0	10	7	0	0	0	0	0	0	0	0	31
OTU_72	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__OM60	g__	s__	4	0	0	2	16	0	24	0	0	2	0	0
OTU_171	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	12	0	3	23	0	1	0	0	2	26	2
OTU_78	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	11	3	0	3	4	0	1	0	0	1	26	0
OTU_291	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	1	2	5	0	0	1	0	0	31	0	0	3
OTU_3456	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	3	1	2	0	0	3	0	0	0	4	0
OTU_795	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	1	1	0	0	3	0	2	2	0	0	0	0
OTU_336	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	8	0	0	1	0	1	0	0	0	2	0
OTU_427	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	0	0	1	0	0	1	0	0	0	3	3
OTU_3710	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	1	0	1	0	0	0	0	0	0	3	0
OTU_377	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	0	0	5	0	0	4	0	0	0	3	0
OTU_847	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	7	0	0	0	0	0	3	0	0	1	0	0
OTU_490	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	2	0	1	2	0	1	0	0	2	0	0
OTU_71	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	16	0	1	0	0	0	37	27	0	0	0	2
OTU_324	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	6	0	0	6	0	3	0	0	1	0	0
OTU_45	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	0	1	0	0	0	45	54	0	0	0	4
OTU_526	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	0	0	1	2	0	3	0	0	1	0	0
OTU_1171	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	1	0	0	0	0	1	0	0	1	0	0
OTU_704	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	8	1	0	0	0	0	0	0	0	1	0
OTU_764	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Ectothiorhodospiraceae	g__	s__	0	8	0	2	0	0	0	0	0	0	3	0
OTU_1956	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__	g__	s__	0	0	0	2	1	0	0	0	0	0	1	0
OTU_39	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Enterobacteriales	f__Enterobacteriaceae	g__Serratia	s__marcescens	4	0	0	0	4	359	0	0	0	1	0	0
OTU_122	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	5	8	1	0	2	0	3	6	0	0	1	6
OTU_259	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	2	33	0	2	5	0	12	20	0	0	13	0
OTU_500	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	0	8	0	1	1	0	1	0	0	0	0	0
OTU_125	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	0	0	1	0	0	0	12	11	0	0	0	0
OTU_1859	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	0	1	0	0	1	0	0	0	0	0	1	0
OTU_362	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__HTCC2188	f__HTCC2089	g__	s__	0	0	3	0	0	0	2	54	0	0	0	0
OTU_382	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Legionellales	f__Francisellaceae	g__Nebulobacter	s__yamanensis	0	0	3	0	1	0	0	0	9	2	0	3
OTU_44	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Legionellales	f__Francisellaceae	g__Fangia	s__hongkongensis	0	0	0	0	0	2	0	0	2	0	0	2
OTU_108	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__	g__	s__	0	0	0	2	0	0	44	0	0	0	0	1
OTU_1147	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Alcanivoracaceae	g__Alcanivorax	s__dieselolei	0	1	1	0	1	0	0	0	0	0	0	0
OTU_14	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	97	234	1872	82	28	121	68	44	832	0	67	524
OTU_54	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	10	0	105	6	4	0	0	0	4	0	1	153
OTU_232	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__Endozoicomonas	s__montiporae	0	0	7	0	1	0	0	0	13	0	0	6
OTU_317	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	2	1	4	0	0	0	0	0	9	0	0	0
OTU_482	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	0	0	19	19	1	0	0	0	0	0	0	3
OTU_1018	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	1	0	0	0	0	0	0	1	0	0	0	1
OTU_3133	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Hahellaceae	g__	s__	0	0	0	3	0	0	0	0	1	0	0	1
OTU_443	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Halomonadaceae	g__Halomonas	s__	0	3	3	0	0	0	0	0	7	0	0	23
OTU_2312	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Halomonadaceae	g__Candidatus Portiera	s__	0	1	0	1	3	0	0	0	0	0	0	0
OTU_350	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Halomonadaceae	g__Candidatus Portiera	s__	0	5	0	0	1	0	5	0	0	0	0	0
OTU_284	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Oceanospirillaceae	g__Amphritea	s__	30	8	1	1	0	0	0	0	0	0	12	2
OTU_1731	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Oceanospirillaceae	g__	s__	0	0	3	1	0	0	0	5	0	2	1	0
OTU_269	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Oceanospirillaceae	g__Neptunomonas	s__	0	11	3	0	0	0	0	0	0	3	0	2
OTU_2503	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Oceanospirillaceae	g__Oleibacter	s__	1	2	0	0	0	2	0	0	0	0	0	0
OTU_1223	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Moraxellaceae	g__Acinetobacter	s__	0	0	1	0	0	0	0	0	0	1	0	2
OTU_36	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Pseudomonadaceae	g__Pseudomonas	s__veronii	109	12	82	0	0	0	1	32	164	0	3	233

OTU_540	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Pseudomonadaceae	g__	s__	0	0	0	0	0	2	0	10	2	0	0	0
OTU_2691	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiolorhabdadales	f__	g__	s__	0	2	0	1	0	0	1	0	0	1	0	0
OTU_279	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiolorhabdadales	f__	g__	s__	3	1	0	5	0	0	4	0	0	0	0	0
OTU_355	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiolorhabdadales	f__	g__	s__	1	0	0	6	8	0	1	0	0	0	0	0
OTU_981	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiolorhabdadales	f__	g__	s__	0	0	0	1	2	0	4	0	0	0	0	0
OTU_351	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiolorhabdadales	f__Piscirickettsiaceae	g__	s__	7	30	1	6	11	1	22	9	0	5	39	4
OTU_13	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	10	14	0	4	6	0	27	3	0	7	6	1
OTU_2909	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	2	10	0	3	0	0	3	9	0	0	16	4
OTU_47	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	23	0	5	0	1	17	8	0	8	9	0
OTU_244	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	3	0	1	0	0	1	5	0	0	1	0
OTU_2524	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	2	0	2	0	0	4	21	0	1	0	0
OTU_137	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	2	11	0	0	3	0	0	0	0	0	1	0
OTU_260	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	18	0	0	5	0	13	0	0	0	0	1
OTU_2633	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	0	0	1	0	0	19	10	0	0	12	0
OTU_308	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	0	0	1	9	1	0	0	0	1	0	0
OTU_356	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	2	0	0	4	0	2	0	0	7	0	0
OTU_405	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	11	0	5	0	0	3	0	0	1	0	0
OTU_898	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	15	0	0	0	0	0	6	0	4	3	0
OTU_2930	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	2	0	0	0	0	4	0	11	0	0	0
OTU_3091	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	2	0	1	1	0	0	0	0	0	0	0
OTU_358	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	2	1	0	0	0	9	0	0	0	0	0
OTU_46	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	0	0	0	14	0	3	0	0	8	0	0
OTU_639	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__	0	5	0	1	0	0	0	0	0	0	1	0
OTU_35	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Pseudoalteromonadaceae	g__Pseudoalteromonas	s__	21	126	77	10	12	24	3	303	54	6	0	37
OTU_198	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Pseudoalteromonadaceae	g__Pseudoalteromonas	s__	147	3	8	0	0	0	0	39	4	1	3	2
OTU_172	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Pseudoalteromonadaceae	g__Pseudoalteromonas	s__	0	11	3	0	0	0	3	14	0	8	0	3
OTU_17	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Vibrio	s__	52	39	420	5	14	1	0	174	1	19	27	402
OTU_2757	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Vibrio	s__	3	0	348	1	2	4	0	26	0	4	3	87
OTU_59	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Photobacterium	s__	2	1	61	0	5	0	0	18	0	8	2	20
OTU_195	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Vibrio	s__	0	3	19	0	0	0	0	0	0	2	1	22
OTU_1925	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Photobacterium	s__	0	0	5	0	0	0	0	1	0	0	1	17
OTU_2257	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Photobacterium	s__damselae	18	2	1	0	0	0	0	0	0	0	0	3
OTU_395	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Vibrio	s__	0	0	8	0	0	1	0	0	0	0	0	2
OTU_56	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Xanthomonadales	f__Xanthomonadaceae	g__Xanthomonas	s__axonopodis	146	3	168	0	0	1	0	0	10	0	1	3
OTU_248	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria					0	1	1	3	0	0	0	0	0	0	3	0
OTU_601	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria					0	1	0	1	0	0	0	0	0	0	2	0
OTU_86	k__Bacteria	p__Proteobacteria						68	0	0	2	0	1	1	277	20	0	2	0
OTU_79	k__Bacteria	p__Proteobacteria						14	0	22	0	1	0	0	0	25	0	0	55
OTU_1908	k__Bacteria	p__Proteobacteria						0	1	1	0	1	0	0	0	0	0	0	0
OTU_70	k__Bacteria	p__SBR1093	c__EC214	o__	f__	g__	s__	1	0	0	0	0	0	28	25	0	0	0	2
OTU_294	k__Bacteria	p__SBR1093	c__EC214	o__	f__	g__	s__	0	1	0	0	1	0	0	0	0	0	2	0
OTU_756	k__Bacteria	p__SBR1093	c__VHS-85-50	o__	f__	g__	s__	0	1	0	2	0	0	1	0	0	0	4	0
OTU_379	k__Bacteria	p__Spirochaetes	c__Spirochaetes	o__Spirochaetales	f__Spirochaetaceae	g__	s__	0	0	0	0	0	0	2	3	0	0	0	1
OTU_442	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mycoplasmatales	f__Mycoplasmataceae	g__Mycoplasma	s__	1	1	0	1	0	0	3	0	0	0	3	1
OTU_2865	k__Bacteria	p__Verrucomicrobia	c__Opitutae	o__Puniceicoccales	f__Puniceicoccaceae	g__Coraliomargarita	s__	0	2	0	0	1	0	0	0	0	1	0	0
OTU_315	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae	o__Verrucomicrobiales	f__Verrucomicrobiaceae	g__Rubritalea	s__	0	10	0	1	0	0	0	7	0	0	4	1
OTU_664	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae	o__Verrucomicrobiales	f__Verrucomicrobiaceae	g__	s__	0	2	1	0	0	0	0	0	0	1	0	0
OTU_753	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae	o__Verrucomicrobiales	f__Verrucomicrobiaceae	g__	s__	0	1	0	0	0	0	1	0	0	0	1	0
OTU_1	k__Bacteria							189	229	341	1081	5	0	807	23	1	37	2489	26
OTU_30	k__Bacteria							8	0	26	0	20	0	5	45	827	0	5	260
OTU_388	k__Bacteria							0	0	0	1	1	0	3	0	0	1	0	0
OTU_1189	k__Bacteria							0	0	0	0	0	0	2	4	0	0	0	3